

Assessing the impact of withering syndrome on the genetic structure of black abalone populations

Christy A. Bell¹, Peter T. Raimondi¹, Giacomo Bernardi¹, Maya George¹, David P. Lohse¹, Steve Lonhart², C. Melissa Miner¹, James D. Moore³, Sara Worden¹

University of California, Santa Cruz¹, Sanctuary Integrated Monitoring Network², California Department of Fish and Game³

Introduction

The black abalone (*Haliotis cracherodii*) has experienced mass mortalities along the coast of California since the mid-1980s and is now a candidate for protection under the USA Endangered Species Act. Mortality is caused by a pathogen that leads to a fatal wasting disease called “withering syndrome” (WS) (Figure 1). Working with MARiNe (Multi-Agency Rocky Intertidal Network) and PISCO (Partnership for Interdisciplinary Studies of Coastal Oceans) monitoring groups, we have documented the northward progression of WS along the California coast. We began monitoring black abalone in 1992 and currently sample 23 sites from Point Conception to Bodega Bay (Figure 2). The last remaining large and healthy populations exist in the Monterey Bay National Marine Sanctuary. Recent declines in the southern portion of the Sanctuary are cause for concern, but whether these declines are due to WS remains to be seen. In this study we couple molecular techniques with ongoing monitoring to work towards answering the following questions:

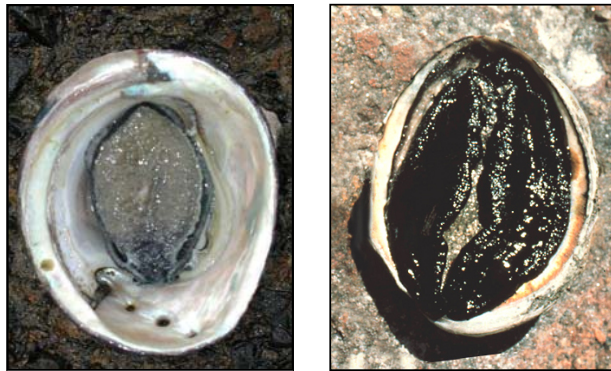


Figure 1. “Withered” black abalone on left. Healthy black abalone on right.

Questions

1. Are the genetic structures of healthy and diseased populations different?
2. If so, to what degree is this genetic difference attributable to “normal” geographic population structure?
3. Does the genetic structure of populations differ before vs after the disease hits?

Acknowledgements

• Funding provided by Packard Ocean Science and Technology Endowment, David and Lucile Packard and Gordon and Betty Moore Foundations (www.piscesweb.org), and Minerals Management Service (www.marine.gov).
 • We would like to thank Karah Cox, Galen Holt, Nick Nesbitt, Bill Henry and many others for their help in the field.
 • We would like to thank Ron Burton's lab at SCRIPPS Institute of Oceanography, especially his student Kristen Gruenthal. Kristen is working on black abalone genetics to address population structure and historical demography.



Figure 2. Map showing locations of sites where black abalone tissue was collected. The percent of population decline due to withering syndrome is shown in orange. The blue dashed line denotes the boundary of the Monterey Bay National Marine Sanctuary.

Methods

In 2005 and 2006, we collected three to four epipodia from individual abalone at six sites using non-lethal techniques (Hamm and Burton 2000) (Figure 3). California Department of Fish and Game provided archived tissue samples collected between 1995 and 2005 from seven sites between Halfmoon Bay and Santa Barbara (Figure 2). Haplotype comparisons were made using the molecular marker Mitochondrial Cytochrome Oxidase 1 (COI). Preliminary analysis was done using ANCOVA and cluster analysis.



Figure 3. Collecting epipodial tissue sample from a healthy black abalone.

Preliminary Findings

From 181 samples, we found 47 different haplotypes (Table 1). When diseased sites were compared to healthy sites, we found no overall reduction in the number of haplotypes (ANCOVA, $P_{\text{value}}=0.8$). Moreover, there was no difference in the composition of haplotypes between healthy and diseased black abalone populations (ANOSIM, $P_{\text{value}} = 0.7$). Thus far, it does not appear that withering syndrome has reduced the haplotypic diversity. However, if withering syndrome continues to spread northward, we should be able to detect any change in genetic diversity. There appears to be no relationship between genetic population structure and geographic location, nor any evidence of temporal patterns (Figure 4). Understanding the relationship between genetic structure and the spatial patterns of abalone populations will help inform management and restoration decision makers regarding this threatened and ecologically important species.

Site	year of crash	year of collection	sample size	# of haplotypes
Pebble Beach	n/a	2005	15	5
Año Nuevo Island*	n/a	1995/1997	4	3
Scott Creek*	n/a	1999	15	8
Scott Creek	n/a	2006	13	5
Monterey*	n/a	1998	16	8
Andrew Molera	n/a	2005	15	9
Andrew Molera	n/a	2006	24	11
Pacific Valley*	n/a	2005	13	5
Point Sierra Nevada	2004	2005	14	8
Diablo Canyon*	1988	1996	4	3
Purisima Point	1998	2006	11	7
Point Arguello*	1995	1997	20	6
Santa Rosa Island*	1988	2005	7	6
Isla Guadalupe	unknown	2005	10	4
Total			181	47

Table 1. Number of haplotypes found at sites where tissue was collected. Sites presented from north to south. Starred sites indicate archived tissue samples. Orange line shows the northern extent of known population declines due to withering syndrome. No monitoring data is available for Isla Guadalupe.

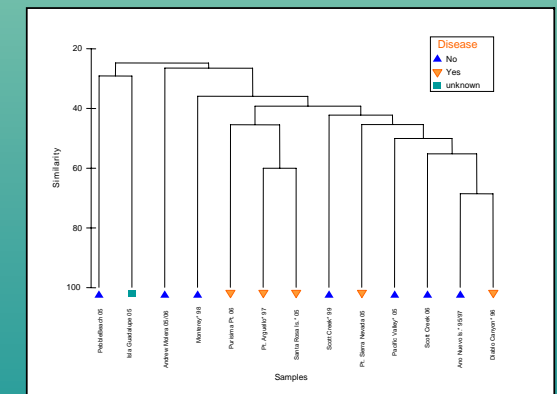


Figure 4. Cluster diagram showing sites grouped by genetic similarity. Starred sites indicate archived tissue samples. Years indicate when samples were collected. Bray-Curtis similarity used. Data were 4th root transformed prior to analysis.

References

Hamm, D.E., Burton, R.S. (2000) Population genetics of black abalone, *Haliotis cracherodii*, along the central California coast. J. Exp. Mar. Biol. Ecol. 254: 235-247.
 PRIMER 6 (2005). PRIMER-E LTD, Plymouth, UK.



For more information contact Christy Bell – roe@biology.ucsc.edu